

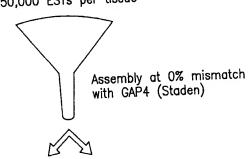


Systematic Gene Search in the Incyte LifeSeq Database Tumor tissue Normal tissue ~50,000 individual ESTs ~50,000 individual ESTs Priority list High Iterative assembling **Prostate** with Breast increasing Ovary mismatch Bladder Uterus Low  $\sim$ 8,000 contigs ~8,000 contigs ~25,000 individual ~25,000 individual sequences sequences Comparison of databases nonspecifically tumor tissue-specific (expected: 100-500) normal tissue-specific (expected: 100-500) expressed genes Genes of Interest

FIG. I

Principle of EST Assembly

~50,000 ESTs per tissue



Contigs increasing in number and length

Contigs increasing in increasing mismatch (1%, 2%, 4%)

5000-6000 Contigs

~25,000 other individual sequences

~30,000 consensussequences per tissue

FIG. 2a

 APPROVED O.G. FIG.

BY Diaftsman

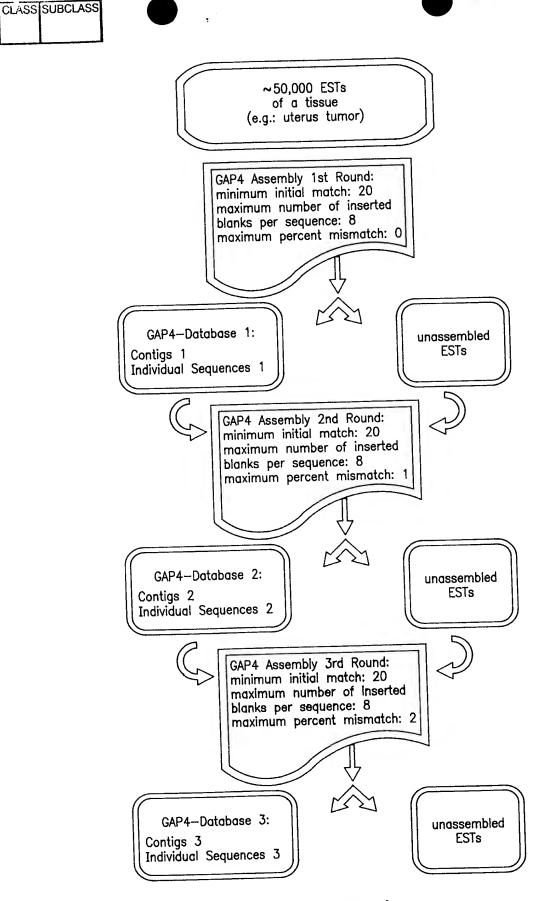


FIG. 2b-I

[A	PPROVED	O.G. FIG.		
	- <b>8</b> Y	CLASS	SUBCLASS	
b	RAFTSMAN			

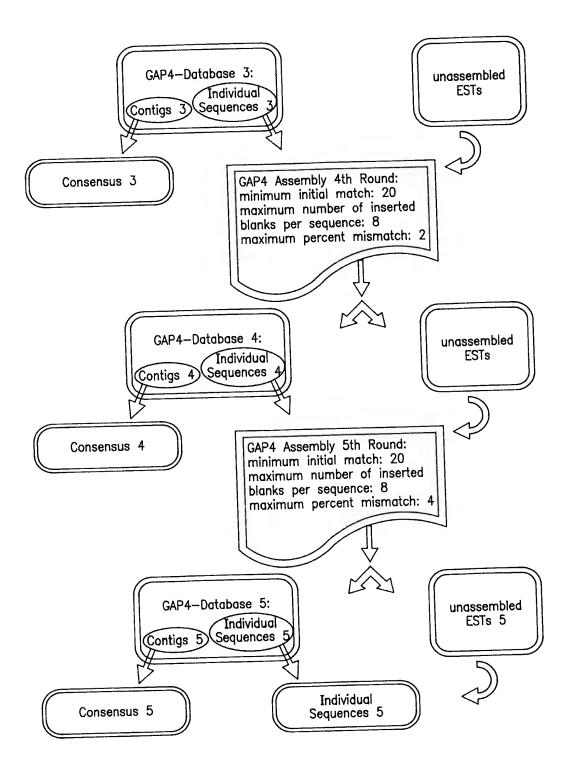


FIG. 2b-2

1	APPROVED	O.G. FIG.		
	₿Y	CLASS	SUBCLASS	
	DRAFTSMAN			

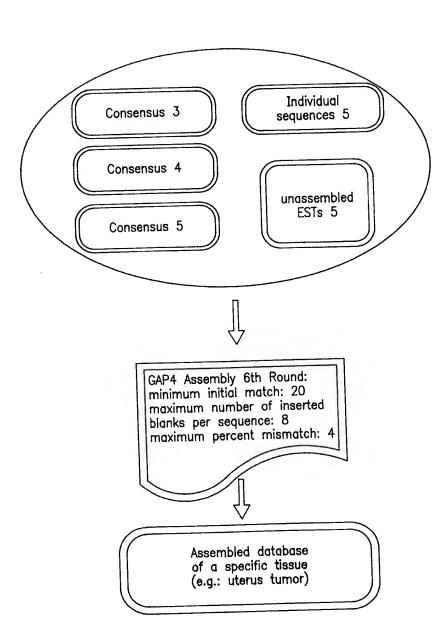


FIG. 2b-3

AFPROVED O G. FIG.

3Y DRAFTSMAN

CLASS SUBCLASS

Assembled database of a specific tissue (e.g.: uterus tumor) Consensus 6 Read-in as individual sequences Database of a second Database specific tissue of a specific tissue (e.g.: normal uterus) (e.g.: uterus tumor) GAP4 Assembly minimum initial match: 20 maximum number of inserted blanks per sequence: 8 maximum percent mismatch: 4 Normal tissue-Non-tissue-Tumor tissuespecific ESTs specific ESTs specific ESTs

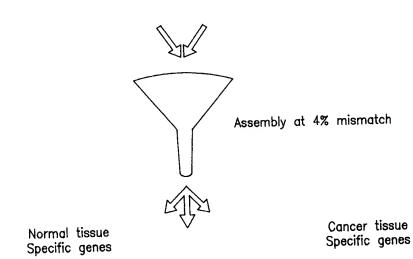
FIG. 2b-4

<b>APPROVED</b>	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences normal tissue

~30,000 consensus sequences tumor tissue



Genes expressed in both tissues

FIG. 3

<b>APPROVED</b>	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

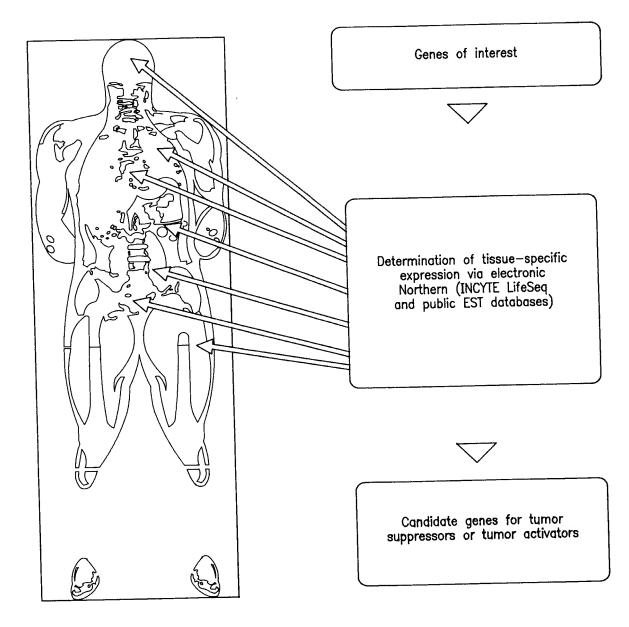


FIG. 4a

APPROVED O.G. FIG.		
BY	CLASS	SUBCLASS
DRAFTSMAN		

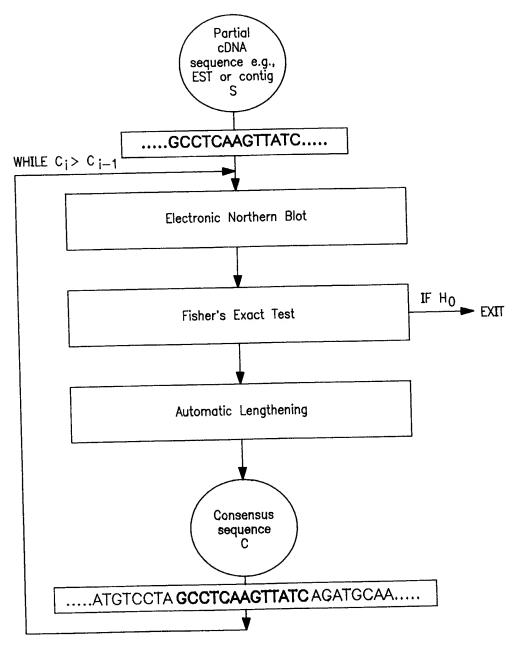
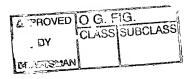


FIG. 4b



Isolation of genomic BAC and PAC clones Chromosomal clone localization via FISH Hybridization signal Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes Intron Exon  $\nabla$ Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

FIG. 5